AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Claim 1 (currently amended): An isolated compound which inhibits pilus assembly**, or a pharmaceutically-acceptable salt thereof**, said compound comprising a mimic of a chaperone G1 beta-strand or a mimic of an amino terminal motif of a pilus subunit, wherein the mimic is a 10 to 20 residue peptide, having an amino terminus and a carboxy terminus, according to formula (I):

~~(I)~~ Z_1~Z_2–X_1–X_2–X_3–X_4–X_5–X_6–X_7–X_8–X_9–X_{10}–Z_3~Z_4 **(I)** ~~or a pharmaceutically-acceptable salt thereof,~~

wherein:

Z_1 is the amino terminus of the mimic peptide, Z_1 having the formula R-C(O)-NR- or RRN-;

Z_2 is (i) a first peptide sequence consisting of 1 to 5 amino acid residues or (ii) a bond connecting Z_1 to X_1;

X_1 is any amino acid residue;

X_2 is any amino acid residue;

X_3 is a hydrophobic residue or a hydroxyl-substituted aliphatic residue;

X_4 is any amino acid residue;

X_5 is a hydrophobic residue or Gly;

X_6 is a hydrophobic or a hydrophilic residue;

X_7 is Gly, an amide-substituted polar residue or a hydrophobic residue;

X_8 is an amino acid residue other than an aliphatic residue;

X_9 is an aliphatic residue;

X_{10} is any amino acid residue;

Z_3 is (i) a second peptide sequence consisting of 1 to 5 amino acid residues or (ii) a bond connecting Z_4 to X_{10};

Z_4 is the carboxy terminus of the peptide, Z4 having the formula –C(O)OR or –C(O)NRR;

each R is independently hydrogen, (C_1-C_6) alkyl, (C_2-C_6) alkenyl, (C_2-C_6) alkynyl or (C_6-C_{14}) aryl;

each "–" between residues X_1 through X_{10}, Z_2 and X_1 and X_{10} and Z_3 independently represents an amide linkage, a substituted amide linkage or an isostere of an amide linkage; and

each "~" represents a bond.

Claim 2-3 (cancelled)

Claim 4 (previously presented): The compound of claim 1 wherein the compound exhibits antibacterial activity against a Gram-negative bacterium.

Claim 5 (currently amended): **An isolated compound which inhibits pilus assembly, said compound comprising SEQ ID NO: 1, wherein the compound is a mimic of a chaperone G_1 beta-strand and the compound exhibits antibacterial activity against a Gram-negative bacterium.** ~~**The compound of claim 4 wherein said mimic comprises SEQ ID NO: 1 or an analog thereof.**~~

Claim 6 (cancelled)

Claim 7 (cancelled)

Claim 8 (previously presented): The compound of claim 1 wherein the compound comprises a mimic of an amino terminal motif of a pilus subunit selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO:

22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28 and SEQ ID NO: 29.

Claim 9 (currently amended): The compound of claim 8 wherein said mimic of an amino-terminal motif of a pilus subunit further comprises the amino acid sequence SDVAFRGNLL (SEQ ID NO: 12) ~~or an analog thereof~~.

Claim 10 (cancelled)

Claim 11 (cancelled)

Claim 12 (cancelled)

Claim 13 (previously presented): The compound of claim 1 wherein one or more of the following conditions are satisfied:

each "–" between residues X_1 through X_{10}, Z_2 and X_1 and X_{10} and Z_3 is an amide linkage;

Z_1 is H_2N–;

Z_4 is –C(O)OH or a salt thereof;

Z_2 is a bond connecting Z_1 to X_1;

Z_3 is a bond connecting Z_4 to X_{10};

X_1 is an amino acid residue other than a basic residue;

X_2 is an amino acid residue other than an aliphatic residue;

X_3 is an aliphatic residue or T;

X_4 is an amino acid residue other than an acidic residue;

X_5 is an aliphatic residue, F or G;

X_7 is G, N or A; or

X_{10} is an aliphatic or a polar residue.

Claim 14 (previously presented): The compound of claim 13 wherein the mimic comprises a sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID

NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28 and SEQ ID NO: 29.

Claim 15 (cancelled)

Claim 16 (currently amended): An isolated compound which inhibits pilus assembly**, or a pharmaceutically-acceptable salt thereof**, the compound comprising a mimic of a chaperone G_1 beta-strand or a mimic of an amino terminal motif of a pilus subunit, wherein the mimic is a 7 to 17 residue peptide ~~or peptide analog~~, having an amino terminus and a carboxy terminus, according to formula (II):

~~(II)~~ Z_{11} ~Z_{12}–X_{11}–X_{12}–X_{13}–X_{14}–X_{15}–X_{16}–X_{17}–Z_{13}~ Z_{14} **(II)**

~~or a pharmaceutically-acceptable salt thereof,~~

wherein:

Z_{11} is the amino terminus of the peptide, Z_{11} having the formula R'–C(O)–NR'– or R'R'N–;

Z_{12} is (i) a first peptide sequence consisting of 1 to 5 amino acid residues or (ii) a bond connecting Z_{11} to X_{11};

X_{11} is any amino acid residue;

X_{12} is any amino acid residue;

X_{13} is a hydrophobic residue;

X_{14} is any amino acid residue;

X_{15} is a hydrophobic residue;

X_{16} is any amino acid residue;

X_{17} is hydrophobic residue or a hydroxyl-substituted aliphatic residue;

Z_{13} is (i) a second peptide sequence consisting of 1 to 5 amino acid residues or (ii) a bond connecting Z_{14} to X_{17};

Z_{14} is the carboxy terminus of the peptide, Z_{14} having the formula –C(O)OR' or –C(O)NR'R';

each R' is independently hydrogen, (C_1-C_6) alkyl, (C_2-C_6) alkenyl, (C_2-C_6) alkynyl or (C_6-C_{14}) aryl;

each "–" between residues X_{11} through X_{17}, Z_{12} and X_{11} and X_{17} and Z_{13} independently represents an amide linkage, a substituted amide linkage or an isostere of an amide linkage; and

each "~" independently represents a bond.

Claim 17 (previously presented): The compound of claim 16 wherein one or more of the following conditions are satisfied:

each "–" between residues X_{11} through X_{17}, Z_{12} and X_{11} and X_{17} and Z_{13} is an amide linkage;

Z_{11} is H_2N–;

Z_{14} is –C(O)OH or a salt thereof;

Z_{12} is a bond connecting Z_{11} to X_{11};

Z_{13} is a bond connecting Z_{14} to X_{17};

X_{11} is an amino acid residue other than a basic residue;

X_{13} is an aliphatic residue or M;

X_{14} is an amino acid residue other than an aromatic residue;

X_{15} is an aliphatic residue, F or M; and

X_{17} is an aliphatic residue, F, M or a hydroxyl-substituted aliphatic residue.

Claim 18 (cancelled)

Claim 19 (currently amended): The compound of any one of claims 1, ~~2,~~ 5, 8, 9, 13, 14, 16, or 17 wherein said compound exhibits antibacterial activity against one or more Gram-negative bacterium selected from the group consisting of *E. coli, H. influenzae, S. euteriditis, S. typhimurium, B. pertussis, Y. pestis, Y. entarocolitica, H. pylori* and *K. pneumoniae*.

Claims 20-135 (cancelled)

Claim 136 (previously presented): An isolated compound which inhibits pilus assembly, the compound consisting of SEQ ID NO: 12.

Claim 137 (previously presented): An isolated compound which inhibits pilus assembly, the compound consisting essentially of SEQ ID NO: 12, wherein the compound is a mimic of an amino terminal motif of a pilus subunit.

Claim 138 (previously presented): An isolated compound which inhibits pilus assembly, the compound comprising a mimic of an amino terminal motif of a pilus subunit, wherein the mimic comprises SEQ ID NO:12.

Claim 139 (previously presented): The compound of claim 138 wherein the compound competitively binds to a pilus subunit hydrophobic groove.

Claim 140-158 (cancelled)

Claim 159 **(new)** The compound of claim 1 wherein the compound consists essentially of a 10 to 20 residue peptide according to formula (I).

Claim 160 **(new)** The compound of claim 16 wherein the compound consists essentially of a 7 to 17 residue peptide according to formula (II).